



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 10000000000000000000

TO: Jeffrey Parkin
Location: rem/3D39/3C18
Art Unit: 1648
Friday, October 28, 2005
Case Serial Number: 09/826115

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523
toby.port@uspto.gov

Search Notes

Examiner Parkin,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

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From: Parkin, Jeffrey
Sent: Thursday, October 20, 2005 1:52 PM
To: STIC-Biotech/ChemLib
Subject: U.S. Serial No. 09/826,115 Sequence Search

Please search **SEQ ID NO.: 14** from U.S. Application No. **09/826,115** v. all relevant databases. Place results on **BOTH** paper and electronic format (i.e., disk, e-mail, etc.).

Thanks!

JSP
REM 3D39
2-0908

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Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Query Match	100.0%	Score 118;	DB 6;	Length 24;	XX	Plasmid pCBD2-14-6 containing dengue-2 virus prM and E.
Best Local Matches	100.0%	Pred. No. 9.4e-11;			XX	Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
Matches 24;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	XX	pCBD2-14-6; dengue virus; DEN-2.
Qy	1 MGKRSAGSIMMLASLAVVIACAGA 24				XX	Unidentified.
Db	1 MGKRSAGSIMMLASLAVVIACAGA 24				OS	Dengue-2 virus.
					OS	Chimeric.
					XX	
RESULT 2					PN	WO200281754-A1.
					XX	
					PD	17-OCT-2002.
					XX	
					PF	04-APR-2002;
					XX	2002WO-US010764.
					PR	04-APR-2001;
					XX	2001US-00826115.
					PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
					PA	
					PI	Chang GJ;
					XX	
					XX	WPI: 2003-058572/05.
					DR	DR N PSDB; ABV7547.
					XX	
					PT	Novel isolated nucleic acid useful as vaccine for preventing flavivirus
					PT	infection, comprises transcriptional unit encoding signal sequence of one
					PT	flavivirus and immunogenic flavivirus antigen of a second flavivirus.
					XX	
					PS	Example 20; Page 157-158; 174pp; English.
					XX	
					CC	The invention relates to a novel nucleic acid comprising a transcriptional unit encoding a signal sequence of a structural protein
					CC	of a first flavivirus and an immunogenic flavivirus antigen of a second
					CC	flavivirus, where the transcriptional unit directs the synthesis of the
					CC	antigen. The polynucleotide of the invention has virucide activity, and
					CC	acts as a vaccine. A composition of the invention has virucide activity, and
					CC	immunising a subject against infection by a flavivirus. The
					CC	polynucleotide is useful as a vaccine for preventing flavivirus
					CC	infection. The sequence represents plasmid pCBD2-14-6, which contains
					CC	dengue-2 virus (DEN-2) prM and E proteins
					XX	
					SQ	Sequence 685 AA;
					CC	Query Match 100.0%; Score 118; DB 6; Length 685;
					CC	Best Local Similarity 100.0%; Pred. No. 3.2e-09;
					CC	Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
					XX	
					Qy	1 MGKRSAGSIMMLASLAVVIACAGA 24
					Db	1 MGKRSAGSIMMLASLAVVIACAGA 24
					RESULT 4	
					ABP57876	
					ID	ABP57876 standard; protein; 685 AA.
					XX	
					AC	ABP57876;
					XX	07-FEB-2003 (first entry)
					DE	Plasmid pCBD2-2J-2-9-1 protein product.
					XX	
					KW	Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
					KW	pCBD2-2J-2-9-1; Japanese encephalitis virus; dengue-2 virus; DEN-2.
					XX	Unidentified.
					OS	Synthetic.
					XX	
					PN	WO200281754-A1.
					XX	
					PD	17-OCT-2002.
					XX	

PF 04-APR-2002; 2002WO-US010764.
 XX
 PR 04-APR-2001; 2001US-00826115.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Chang GJ;
 XX
 WPI: 2003-058572/05.
 DR N-PSDB; ABV77549.
 XX
 PT Novel isolated nucleic acid useful as vaccine for preventing flavivirus
 PT infection, comprises transcriptional unit encoding signal sequence of one
 PT flavivirus and immunogenic flavivirus antigen of a second flavivirus.
 XX
 PS Example 20; Page 168-169; 174pp; English.
 XX
 CC The invention relates to a novel nucleic acid comprising a
 CC transcriptional unit encoding a signal sequence of a structural protein
 CC of a first flavivirus and an immunogenic flavivirus antigen of a second
 CC flavivirus, where the transcriptional unit directs the synthesis of the
 CC antigen. The Polynucleotide of the invention has virucide activity, and
 CC acts as a vaccine. A composition of the invention is useful for
 CC immunising a subject against infection by a flavivirus. The
 CC polynucleotide is useful as a vaccine for preventing flavivirus
 CC infection. The sequence represents plasmid pCB9D2-IJ-4-3, which contains
 CC dengue-2 virus (DEN-2) prM, M and E, and Japanese encephalitis virus E
 CC proteins
 XX
 SQ Sequence 685 AA;
 CC Query Match 100.0%; Score 118; DB 6; Length 685;
 CC Best Local Similarity 100.0%; Pred. No. 3.2e-09;
 CC Matches 24; Conservative 0; Mismatches 0; N mismatches 0;
 CC Indels 0; Gaps 0;
 CC
 Qy 1 MGKRSAGSIMWLASLAVIACAGA 24
 Db 1 MGKRSAGSIMWLASLAVIACAGA 24
 XX
 RESULT 6
 ABP57859
 ID ABP57859 standard; protein; 692 AA.
 XX
 AC ABP57859;
 XX
 DT 07-FEB-2003 (First entry)
 XX
 DE Plasmid pCBWN containing West nile virus prM and E.
 XX
 KW Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
 KW PCBWN; West nile virus.
 XX
 Unidentified.
 OS West nile virus.
 OS
 XX
 PN WO200281754-A1.
 XX
 DT 17-OCT-2002.
 XX
 DE Plasmid pCB9D2-IJ-4-3 protein product.
 XX
 KW Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
 KW pCB9D2-IJ-4-3; Japanese encephalitis virus; dengue-2 virus; DEN-2.
 XX
 Unidentif.ed.
 OS Synthetic.
 XX
 PN WO200281754-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 04-APR-2002; 2002WO-US010764.
 XX
 PR 04-APR-2001; 2001US-00826115.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Chang GJ;
 XX
 DR WPI: 2003-058572/05.
 XX
 PT Novel isolated nucleic acid useful as vaccine for preventing flavivirus
 PT infection, comprises transcriptional unit encoding signal sequence of one
 PT flavivirus and immunogenic flavivirus antigen of a second flavivirus.
 XX
 PS Example 9; Page 124-125; 174pp; English.
 XX
 CC The invention relates to a novel nucleic acid comprising a
 CC transcriptional unit encoding a signal sequence of a structural protein
 CC of a first flavivirus and an immunogenic flavivirus antigen of a second
 CC flavivirus, where the transcriptional unit directs the synthesis of the
 CC antigen. The Polynucleotide of the invention has virucide activity, and
 CC acts as a vaccine. A composition of the invention is useful for
 CC immunising a subject against infection by a flavivirus. The
 CC polynucleotide is useful as a vaccine for preventing flavivirus

CC infection. The sequence represents plasmid PCBWN, which contains West
 CC nile virus prM and E proteins
 XX

SQ Sequence 692 AA;

Query Match 100.0%; Score 118; DB 6; Length 692;
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKRSAGSIMMLASLAVIACAGA 24
 Db 1 MGKRSAGSIMMLASLAVIACAGA 24

RESULT 7
 ABP57864
 ID ABP57864 standard; peptide; 24 AA.
 XX
 AC ABP57864;
 XX DT 07-FEB-2003 (first entry)
 DE St. Louis encephalitis virus JE signal peptide.
 XX Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
 KW St. Louis encephalitis virus; JE signal.
 XX OS St. Louis encephalitis virus.
 XX PN WO200281754-A1.
 XX PD 17-OCT-2002.
 XX PP 04-APR-2002; 2002WO-US010764.
 XX PR 04-APR-2001; 2001US-00826115.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 KW PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Chang GJ;
 XX DR WPI; 2003-058572/05.
 XX N-PSDB; ABV77540.

FT Novel isolated nucleic acid useful as vaccine for preventing flavivirus
 PT infection, comprises transcriptional unit encoding signal sequence of one
 PT flavivirus and immunogenic flavivirus antigen of a second flavivirus.
 FS Example 14; Page 147-148; 174pp; English.

CC The invention relates to a novel nucleic acid comprising a
 CC transcriptional unit encoding a signal sequence of a structural protein
 CC of a first flavivirus and an immunogenic flavivirus antigen of a second
 CC flavivirus, where the transcriptional unit directs the synthesis of the
 CC antigen. The polynucleotide of the invention has virucide activity, and
 CC acts as a vaccine. A composition of the invention is useful for
 CC immunising a subject against infection by a flavivirus. The
 CC polynucleotide is useful as a vaccine for preventing flavivirus
 CC infection. The sequence represents Plasmid PCBWF, which contains Yellow
 CC fever virus prM and E proteins
 XX SQ Sequence 681 AA;

Query Match . Score 96; DB 6; Length 681;
 Best Local Similarity 87.5%; Pred. No. 7.3e-06;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGKRSAGSIMMLASLAVIACAGA 24
 Db 1 MGKRSAGSIMMLASLAVIAGTSA 24

RESULT 9
 ABP57861
 ID ABP57861 standard; peptide; 681 AA.
 XX AC ABP57861;
 XX DT 07-FEB-2003 (first entry)
 DE Plasmid PCBPOW containing Powassan virus prM and E.
 XX DB Plasmid PCBPOW containing Powassan virus prM and E.
 KW Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
 KW PCBPOW; Powassan virus.
 XX OS Unidentified.
 OS Powassan virus.

RESULT 8
 ABP57863

OS Chimeric.
 XX PN WO200281754-A1.
 PD 17-OCT-2002.
 XX PP 04-APR-2002; 2002WO-US010764.
 XX PR 04-APR-2001; 2001US-00826115.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Chang GJ;
 XX DR WPI; 2003-058572/05.
 XX N-PSDB; ABV77539.
 PT Novel isolated nucleic acid useful as vaccine for preventing flavivirus infection, comprises transcriptional unit encoding signal sequence of one flavivirus and immunogenic flavivirus antigen of a second flavivirus.
 XX PS Example 13; Page 141-142; 174pp; English.
 XX The invention relates to a novel nucleic acid comprising a transcriptional unit encoding a signal sequence of a structural protein of a first flavivirus and an immunogenic flavivirus antigen of a second flavivirus, where the transcriptional unit directs the synthesis of the antigen. The polynucleotide of the invention has virucide activity, and acts as a vaccine. A composition of the invention is useful for immunising a subject against infection by a flavivirus. The polynucleotide is useful as a vaccine for preventing flavivirus infection. The sequence represents Plasmid pCBJESS-M, which contains St. Louis encephalitis virus prM and E proteins.
 XX SQ Sequence 692 AA;
 XX Query Match 81.4%; Score 96; DB 6; Length 692;
 XX Best Local Similarity 87.5%; Pred. No. 7.4e-06;
 XX Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 MGKRSAGSIMWLASIIVIACAGA 24
 Db 1 MGKRSAGSIMWLASIIVIAGTSA 24
 XX RESULT 11
 ABP57879 standard; peptide; 39 AA.
 XX ID ABP57879
 XX AC ABP57879;
 XX DT 07-FEB-2003 (first entry)
 XX DE Signal sequence preceding prM protein in plasmid pCBJEB1-14.
 XX KW Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
 XX KW signal sequence.
 XX OS Unidentified.
 XX PN WO200281754-A1.
 XX PD 17-OCT-2002.
 XX PP 04-APR-2002; 2002WO-US010764.
 XX PR 04-APR-2001; 2001US-00826115.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Chang GJ;
 XX DR WPI; 2003-058572/05.
 PT Novel isolated nucleic acid useful as vaccine for preventing flavivirus infection, comprises transcriptional unit encoding signal sequence of one flavivirus and immunogenic flavivirus antigen of a second flavivirus.
 XX PS Disclosure; Fig 6; 174pp; English.
 XX The invention relates to a novel nucleic acid comprising a transcriptional unit encoding a signal sequence of a structural protein of a first flavivirus and an immunogenic flavivirus antigen of a second flavivirus, where the transcriptional unit directs the synthesis of the antigen. The polynucleotide of the invention has virucide activity, and

CC acts as a vaccine. A composition of the invention is useful for
 CC immunising a subject against infection by a flavivirus. The
 CC polynucleotide is useful as a vaccine for preventing flavivirus
 CC infection. The sequence represents the signal sequence preceding the prM
 CC protein in the plasmid PCBJE1-14 of the invention

SQ Sequence 39 AA;
 Query Match 77.1%; Score 91; DB 6; Length 39;
 Best Local Similarity 66.7%; Pred. No. 2.1e-06;
 Matches 20; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
 Qy 1 MGKR-----SAGSIMWLASLAVIACAGA 24
 Db 1 MGRKQNKRGGNEGSIMWLASLAVIACAGA 30

RESULT 12
 ABP57860
 ID ABP57860 standard; protein; 697 AA.
 XX
 AC ABP57860;
 XX
 DT 07-FEB-2003 (first entry)
 XX
 DE Plasmid PCBJE1-14 containing Japanese encephalitis virus prM and E.
 XX
 DE Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
 KW PCBJE1-14; Japanese encephalitis virus.
 XX
 OS Unidentified.
 OS Japanese encephalitis virus.
 OS Chimeric.
 XX
 PN WO200281754-A1.
 XX
 PD 17-OCT-2002.
 XX
 PR 04-APR-2002; 2002WO-US010764.
 XX
 PR 04-APR-2001; 2001US-00826115.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Chang GJ;
 XX
 WPI; 2003-058572/05.
 DR N-PSDB; ABV77533.
 XX
 PT Novel isolated nucleic acid useful as vaccine for preventing flavivirus
 PT infection, comprises transcriptional unit encoding signal sequence of one
 PT flavivirus and immunogenic flavivirus antigen of a second flavivirus.
 XX
 PS Example 1; Page 117-119; 174pp; English.

XX
 PR 04-APR-2001; 2001US-00826115.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES
 XX
 PD 17-OCT-2002.
 XX
 PR 04-APR-2002; 2002WO-US010764.
 XX
 PR 04-APR-2001; 2001US-00826115.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES
 XX
 PI Chang GJ;
 XX
 DR WPI; 2003-058572/05.
 DR N-PSDB; ABV77533.
 XX
 PT Novel isolated nucleic acid useful as vaccine for preventing flavivirus
 PT infection, comprises transcriptional unit encoding signal sequence of one
 PT flavivirus and immunogenic flavivirus antigen of a second flavivirus.
 XX
 PS Example 1; Page 130-131; 174pp; English.

XX
 CC The invention relates to a novel nucleic acid comprising a
 CC transcriptional unit encoding a signal sequence of a structural protein
 CC of a first flavivirus and an immunogenic flavivirus antigen of a second
 CC flavivirus, where the transcriptional unit directs the synthesis of the
 CC antigen. The polynucleotide of the invention has virucide activity, and
 CC acts as a vaccine. A composition of the invention is useful for
 CC immunising a subject against infection by a flavivirus. The
 CC polynucleotide is useful as a vaccine for preventing flavivirus
 CC infection. The present sequence represents the Japanese encephalitis
 CC virus prM and E proteins

SQ Sequence 697 AA;
 Query Match 77.1%; Score 91; DB 6; Length 697;
 Best Local Similarity 66.7%; Pred. No. 4.3e-05;
 Matches 20; Conservative 3; Mismatches 1; Indels 6; Gaps 1;
 Qy 1 MGKR----SAGSIMWLASLAVIACAGA 24
 Db 1 MGRKQNKRGGNEGSIMWLASLAVIACAGA 30

RESULT 14
 ADM97134
 ID ADM97134 standard; peptide; 23 AA.
 XX
 AC ADM97134;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Japanese-encephalitis-virus signal peptide.
 XX
 KW Japanese-encephalitis-virus; antigen; M protein; E protein;
 Qy 1 MGKR-----SAGSIMWLASLAVIACAGA 24

SQ Sequence 39 AA;
 Query Match 77.1%; Score 91; DB 6; Length 697;
 Best Local Similarity 66.7%; Pred. No. 4.3e-05;
 Matches 20; Conservative 3; Mismatches 1; Indels 6; Gaps 1;
 Qy 1 MGKR-----SAGSIMWLASLAVIACAGA 30

RESULT 13
 ABP57857
 ID ABP57857 standard; protein; 697 AA.
 XX
 AC ABP57857;
 XX
 DT 07-FEB-2003 (first entry)
 XX
 DE Japanese encephalitis virus prM and E proteins.
 XX
 DE Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
 KW Japanese encephalitis virus.
 XX
 OS Japanese encephalitis virus.
 XX
 PN WO200281754-A1.
 XX
 PD 17-OCT-2002.
 XX
 PR 04-APR-2002; 2002WO-US010764.
 XX
 PR 04-APR-2001; 2001US-00826115.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Chang GJ;
 XX
 DR WPI; 2003-058572/05.
 DR N-PSDB; ABV77533.
 XX
 PT Novel isolated nucleic acid comprising a signal sequence of one
 PT flavivirus and an immunogenic flavivirus antigen of a second
 PT flavivirus, where the transcriptional unit directs the synthesis of the
 PT antigen. The polynucleotide of the invention has virucide activity, and
 PT acts as a vaccine. A composition of the invention is useful for
 PT immunising a subject against infection by a flavivirus. The
 PT polynucleotide is useful as a vaccine for preventing flavivirus
 PT infection. The present sequence represents the Japanese encephalitis
 PT virus prM and E proteins

SQ Sequence 697 AA;
 Query Match 77.1%; Score 91; DB 6; Length 697;
 Best Local Similarity 66.7%; Pred. No. 4.3e-05;
 Matches 20; Conservative 3; Mismatches 1; Indels 6; Gaps 1;
 Qy 1 MGKR----SAGSIMWLASLAVIACAGA 24
 Db 1 MGRKQNKRGGNEGSIMWLASLAVIACAGA 30

KW haemagglutination; beta-actin promoter; vaccine.
 XX Japanese encephalitis virus.
 OS
 XX
 PN JP200406518-A.
 XX
 PD 04-MAR-2004.
 XX
 PF 07-AUG-2002; 2002JP-00229597.
 XX
 PR 07-AUG-2002; 2002JP-00229597.
 XX
 PT Novel Japanese encephalitis-virus antigen comprising Japanese-
 encephalitis-virus-like particle consisting of M and E protein, useful as
 PT Japanese-encephalitis-virus vaccine.
 PA (HAND-) ZH HAN DAI BISEIBUTSUBYO KENKYUKAI.
 PA (KOKU-) KOKURITSU YODO EIsei KENKYUSHO.
 XX
 DR WPI; 2004-209123/20.
 DR N-PSDB; AUM97133.
 XX
 PT Novel Japanese encephalitis-virus antigen comprising Japanese-
 encephalitis-virus-like particle consisting of M and E protein, useful as
 PT Japanese-encephalitis-virus vaccine.
 PS Disclosure; SEQ ID NO 5; 45pp; Japanese.
 XX
 CC The invention relates to a novel Japanese-encephalitis-virus antigen
 comprising a Japanese-encephalitis-virus-like particle, which includes
 the M protein and E protein of a Japanese encephalitis virus, and which
 CC does not contain RNA in the particle, and shows haemagglutination
 CC activity. The invention further comprises: a transformed cell obtained by
 CC providing cDNA encoding the E protein and prM protein prepared from the
 CC genome RNA of a Japanese-encephalitis virus, preparing a recombinant DNA
 CC by integrating the cDNA in an expression vector which contains a beta-
 CC actin promoter and which can be expressed, transforming an animal cell by
 CC the recombinant DNA, selecting the transformed cell from a parent cell
 CC and making the transformed cell to acclimatize in serum free medium;
 CC Japanese-encephalitis-vaccine having immunity for the novel antigen and
 CC containing the antigen as an active ingredient; and a diagnostic agent
 CC which contains the antigen as an active ingredient. The Japanese-
 CC encephalitis-virus antigen is useful for carrying out the preparation of
 CC a Japanese-encephalitis vaccine and a diagnostic agent. This sequence
 CC represents the Japanese-encephalitis-virus signal peptide of the
 CC invention.
 XX
 SQ Sequence 23 AA:
 Query Match 75.4%; Score 89; DB 8; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.4e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 GSIMWLASLAVVIACAGA 24
 Db 6 GSIMWLASLAVVIACAGA 23
 RESULT 15
 ABP57867
 ID ABP57867 standard; Peptide; 30 AA.
 XX
 AC ABP57867;
 XX
 DT 07-FEB-2003 (first entry)
 XX
 DB Signal sequence preceding prM protein in plasmid PCJEME.
 XX Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
 KW signal sequence.
 XX Unidentified.
 XX
 PN WO200281734-A1.
 XX
 PD 17-OCT-2002.
 XX

PF 04-APR-2002; 2002WO-US010764.
 XX
 PR 04-APR-2001; 2001US-00826115.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Chang GJ;
 XX
 WPI; 2003-058572/05.
 XX
 DR Novel isolated nucleic acid useful as vaccine for preventing flavivirus
 PT infection, comprises transcriptional unit encoding signal sequence of one
 PT flavivirus and immunogenic flavivirus antigen of a second flavivirus.
 PA Example 20; Page 87; 174pp; English.
 XX
 DR The invention relates to a novel nucleic acid comprising a
 CC transcriptional unit encoding a signal sequence of a structural protein
 CC of a first flavivirus and an immunogenic flavivirus antigen of a second
 CC flavivirus, where the transcriptional unit directs the synthesis of the
 CC antigen. The polynucleotide of the invention has virucide activity, and
 CC acts as a vaccine. A composition of the invention is useful for
 CC immunising a subject against infection by a flavivirus. The
 CC polynucleotide is useful as a vaccine for preventing flavivirus
 CC infection. The sequence represents the signal sequence preceding the prM
 CC protein in the plasmid PCJEME of the invention.
 XX
 SQ Sequence 30 AA:
 Query Match 75.4%; Score 89; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 GSIMWLASLAVVIACAGA 24
 Db 4 GSIMWLASLAVVIACAGA 21
 Search completed: October 26, 2005, 01:31:37
 Job time : 167 secs

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RESULT 3							
GNWVJS							
Genome polyprotein - Japanese encephalitis virus (strain SA-14)							
F;1302-1432/Product: nonstructural protein NS2b #status predicted <N2B>							
F;1433-1440/Product: nonstructural protein NS3 (fragment) #status predicted <NS3>							
Matches 18; Binding site: carbohydrate (Asn) (covalent) #status predicted							
Query Match 75.4%; Score 89; DB 1; Length 1440;							
Best Local Similarity 100.0%; Pred. No. 6.3e-05;							
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Qy 7 GSIMMINASLAVVIACAGA 24							
Db 36 GSIMMINASLAVVIACAGA 53							
RESULT 4							
GNWVJE							
Genome polyprotein - Japanese encephalitis virus (strain Jat0ArS982 wild type)							
F;1138-1212/Product: nonstructural protein NS4a #status predicted <N4A>							
F;1209-1297/Product: transmembrane #status predicted <TM>							
Matches 18; Binding site: membrane protein NS4b #status predicted <NS4b>							
Query Match 75.4%; Score 89; DB 1; Length 1432;							
Best Local Similarity 100.0%; Pred. No. 0.00013;							
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Qy 7 GSIMMINASLAVVIACAGA 24							
Db 110 GSIMMINASLAVVIACAGA 127							

A;Title: Complete nucleotide sequence of the Japanese encephalitis virus genome RNA	A;Reference number: A94337; MUID:88072090; PMID:3656827
A;Accession: A27403	
A;Molecule type: genomic RNA	
A;Residues: 1-1342 <SUM>	
A;Cross-references: UNIPROT:P32886; GB:MI18370; NID:9331329; PID:AAA81554.1; PID:G331	
A;Residues: 1-1342 <SUM>	
A;Experimental source: isolate JaotarS982	
A;Notes: sequence extracted from NCBI backbone (NCBIN:109245, NCBIP:109246)	
C;Superfamily: Yellow fever virus genome polyprotein	
C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein	
F;44-60/Domain: transmembrane #status predicted <CAP>	
F;112-127/Product: capsid protein C #status predicted <CAP>	
F;112-127/Domain: transmembrane #status predicted <IN1>	
F;112-127/Domain: transmembrane #status predicted <TN2>	
F;128-294/Product: membrane protein M precursor #status predicted <GLC>	
F;128-294/Domain: nonterminal signal sequence #status predicted <SIG>	
F;220-294/Product: membrane protein M #status predicted <GLM>	
F;280-294/Domain: transmembrane #status predicted <TM3>	
F;295-794/Product: envelope protein B #status predicted <ENV>	
F;776-790/Domain: transmembrane #status predicted <TN4>	
F;795-1206/Product: nonstructural protein NS1 #status predicted <NS1>	
F;1207-1373/Domain: nonstructural protein NS2a #status predicted <N2A>	
F;1374-1504/Product: nonstructural protein NS2b #status predicted <N2B>	
F;1505-2123/Product: nonstructural protein NS3 #status predicted <NS3>	
F;1678-1705/Region: nucleotide-binding motif A (P-loop)	
F;1759-1790/Region: nucleotide-binding motif B	
F;2114-2412/Product: nonstructural protein NS4a #status predicted <N4A>	
F;2413-2527/Product: nonstructural protein NS4b #status predicted <N4B>	
F;288-3424/Product: nonstructural protein NS5 #status predicted <NS5>	
F;1425,448,924/2001,1594/1950,2463,2491,2761,2866,2904/Binding site: carbohydrate (As	
Query Match 66.1%; Score 78; DB 1; Length 3432;	
Best Local Similarity 94.4%; Pred. No. 0.0051;	
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy 7 GSIMWILASLAVVIACAGA 24	
Db 110 GSIMWILASLAVVIAYAGA 127	
RESULT 5	
AF3614 probable undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase (EC 2.4.1.-)	
C;Species: Brucella melitensis	
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004	
C;Accession: AF3614	
R;DeVecchio, V.; Kapartal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov, B.; Mazur, M.; Goltzman, E.; Seikov, E.; Bizer, P.H.; Hagius, S.; O'Callaghan, D.; Lee, J.; Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002	
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis	
A;Reference number: AD3232; PMID:1756688	
A;Accession: AF3614	
A;Molecule type: DNA	
A;Status: preliminary	
A;Map Position: II	
A;Genes: BMS1039	
A;Keywords: glycosyltransferase; hexosyltransferase	
Query Match 44.9%; Score 53; DB 2; Length 354;	
Best Local Similarity 38.9%; Pred. No. 3 5;	
Matches 14; Conservative 1; Mismatches 7; Indels 14; Gaps 1;	

Qy 2 GKRSGASIMWIA-----SLAVVIACAG 23
 Db :||| :||| :||| :||| :||| :||| :|||
 153 GSASASSEPNIAVISDIGHRIGLGSQSLAVVIACAG 188

RESULT 6
 A9106 probable transport system permease protein Ec83017 [imported] - Escherichia coli (strain C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C;Accession: A9106
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Yokoyama, K.; Han, C.G.;gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.;DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: A9106
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-385 <STO>
 A;Cross-references: UNIPROT:Q8X670; GB:BA000007; PIDN:BAB36440_1; PID:gi13362486; GSPDB:G
 A;Experimental source: strain O157:H7, substrate RIMD 0509552
 A;Gene: Ec83017

Query Match 44.9%; Score 53; DB 2; Length 385;
 Best Local Similarity 41.7%; Pred. No. 37; Matches 9; Indels 0; Gaps 0;

Qy 1 MGKRSAGSIMWIA-----SLAVVIACAGA 24
 Db :||| :||| :||| :||| :||| :|||
 103 LARTSLGSFPLASALLACSDA 126

RESULT 7
 B85550 probable transport system permease protein yehY [imported] - Escherichia coli (strain O1
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C;Accession: B85550
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; MUID:11206551
 A;Accession: B85550
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-385 <STO>
 A;Cross-references: UNIPROT:Q8X670; GB:AB005174; PIDN:912516435; PIDN:AA57262_1; GSPDB:G
 A;Experimental source: strain O157:H7, substrate EDL933
 A;Genetics:
 A;Gene: yehY

Query Match 44.9%; Score 53; DB 2; Length 385;
 Best Local Similarity 41.7%; Pred. No. 37; Matches 9; Indels 0; Gaps 0;

Qy 1 MGKRSAGSIMWIA-----SLAVVIACAGA 24
 Db :||| :||| :||| :||| :||| :|||
 103 LARTSLGSFPLASALLACSDA 126

RESULT 8
 G96636 hypothetical protein F11P17_17 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: G96636
 R;Theoelos, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.J.;
 anson, N.F.; Hughes, B.; Huizar, L.; Nature 408, 816-820, 2000

Query Match 43.2%; Score 51; DB 2; Length 485;
 Best Local Similarity 41.7%; Pred. No. 8.8;
 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MGKRSAGSIMWIA-----SLAVVIACAGA 24
 Db :||| :||| :||| :||| :||| :|||
 401 LGAAVQGGMWLAIGVCAVIGA 424

RESULT 10
 T3387 probable integral membrane protein - Streptomyces coelicolor
 C;Species: Streptomyces coelicolor

C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
 C;Accession: T4987
 R;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, August 1998
 A;Reference number: Z21550
 A;Accession: T4987
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-59 <OLI>
 A;Cross-references: UNIPROT:086668; EMBL:AL031182; PIDN:CAA20164.1; GSPDB:GN00070; SCOED
 A;Experimental source: strain A3 (2)
 C;Genetics: SCOEDB:SC4A2.12

RESULT 11
 A64981
 yeh protein - Escherichia coli (strain K-12)
 C;Species: Escherichia coli
 C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
 R;Blattner, F.R.; Plunkett III, G.; Perna, N.T.; Burland, V.; Riley, M.; Co
 .A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1433-1462, 1997
 A;Title: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: A64720; PMID:9426617; PMID:9278503
 A;Accession: A4981
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-85 <BLAT>
 A;Cross-references: UNIPROT:P33361; GB:AE000302; GB:U00096; NID:91788447; PIDN: AAC75191.
 A;Experimental source: strain K-12; substrate MG1655
 C;Genetics: yehY

Query Match 42.4%; Score 50; DB 2; Length 299;
 Best Local Similarity 41.7%; Pred. No. 8.3;
 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 Qy 1 MGKRSAGSIMMLASLAVVIACAGA 24
 Db 238 LGDRPRSGLWMLARGVAAVAGA 261

RESULT 13
 C97866
 hypothetical protein RC1331 [imported] - Rickettsia conorii (strain Malish 7)
 C;Species: Rickettsia conorii
 C;Accession: C97866
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
 Science 293, 2093-2098, 2001
 A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
 A;Reference number: A97700; MUID:21442074; PMID:1155793
 A;Accession: C97866
 A;Status: preliminary
 A;Cross-references: UNIPROT:Q92FZ6; GB:AE006914; PIDN:AA03869.1; PID:915620473; GSPDB:G
 A;Gene: RC1331

RESULT 14
 D65118
 pantothenate permease [validated] - Escherichia coli (strain K-12)
 N;Alternate names: sodium/pantothenate symporter
 C;Species: Escherichia coli
 C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 .A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: A64720; PMID:97426617; PMID:278503
 A;Accession: D65118
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-485 <BLAT>
 A;Cross-references: UNIPROT:Q8X9B1; GB:AE000404; GB:U00096; NID:92367207; PIDN: AAC76290.1
 A;Experimental source: strain K-12; Substrain MG1655
 R;Jackowski, S.; Alix, J-H.
 J.;Bacteriol. 172, 3842-3848, 1990
 A;Title: Cloning, sequence, and expression of the pantothenate permease (panF) gene of E.
 coli: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: JU0296; MUID:90299808; PMID:2193919
 A;Accession: JU0296
 A;Molecule type: DNA
 A;Residues: 3-180; APAABRH' 207-208; 'RACDADWHRCAAYWRSTC' 209-255; 'A' 257-303; 'H' 305-485
 A;Cross-references: GB:M30953; NID:9147066; PIDN:AAA24276.1; PMID:9147067
 A;Experimental source: strain K12
 R;Vanat, A.; Plumbridge, J.A.; Alix, J.H.
 J.;Bacteriol. 175, 7178-7188, 1993
 A;Title: Cotranscription of two genes necessary for ribosomal protein L11 methylation (p
 A;Reference number: A49924; MUID:9042890; PMID:8226664
 A;Accession: A49924
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 445-485 <VAN>
 A;Cross-references: GB:S67010; NID:9455653; PIDN: AAB28768.1; PMID:9455654

RESULT 12
 H71346
 hypothetical protein T0259 - syphilis spirochete
 C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A;Reference number: A71250; MUID:90332770; PMID:9665876
 A;Accession: H71346
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-103 <COL>
 A;Cross-references: UNIPROT:083283; GB:AE001207; GB:AE000520; NID:93322526; PIDN: AAC6525
 A;Experimental source: strain Nichols
 C;Gene: T0259
 C;Superfamily: syphilis spirochete hypothetical protein T0259

A; Experimental source: strain K12
 A; Note: sequence extracted from NCBI backbone (NCBIN:139766, NCBIP:139767)
 C; Genetics:
 A; Gene: panF
 C; Function:
 A; Description: catalyzes the sodium-dependent uptake of extracellular pantothenate [vali
 C; Superfamily: proline carrier protein
 C; Keywords: sodium transport; symport system; transmembrane protein

Query 9 MMWLASLAVVACAGA 24
 ::|||||:|||||:
 Db 125 LWLASLIVAFVGA 140

RESULT 15

P85990 sodium/pantothenate symporter [imported] - Escherichia coli (strain O157:H7, substrain E
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C;Accession: P85990
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grobeck, B.J.; Davis, N.W.; Lim, A.; Dimlaanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; PMID:21074935; PMID:11206551
 A;Accession: P85990
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-485 <STO>
 A;Cross-references: UNIPROT:Q8X9B1; GB:AE005174; NID:G12517885; PIDN:AAG58386.1; GSPDB:G

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: panF

C;Superfamily: proline carrier protein

Query 9 MMWLASLAVVACAGA 24
 ::|||||:|||||:
 Db 125 LWLASLIVAFVGA 140

Search completed: October 26, 2005, 01:35:14
 Job time : 40 secs

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Scoring table: BL05UM62							Alignments						
Searched: 1612378 seqs, 512079187 residues							Result 1						
Total number of hits satisfying chosen parameters: 1612378							ID 082863 PRELIMINARY; PRT; 789 AA.						
Minimum DB seq length: 0	AC 082863;						AC 082863;	01-NOV-1996	(TrEMBLrel. 01, Created)				
Maximum DB seq length: 2000000000	DT 01-MAR-2004	(TrEMBLrel. 01, Last sequence update)					DT 01-MAR-2004	(TrEMBLrel. 26, Last annotation update)					
Post-processing: Minimum Match 0%	DE Polyprotein (Fragment).						DE Polyprotein (Fragment).						
Maximum Match 100%	OS Japanese encephalitis virus.						OS Japanese encephalitis virus.						
Listing First 45 summaries	OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;						OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;						
Database :	NCBI_TaxID=11072;						NCBI_TaxID=11072;						
1: uniprot_sprot;*	OX						OX						
2: uniprot_trembl;*	RN [1] -	RP SEQUENCE FROM N.A.					RN [1] -	RP SEQUENCE FROM N.A.					
Scoring table: BL05UM62	RC STRAIN=8256;						RC STRAIN=8256;						
Gapop 10.0 , Gapext 0.5	RX MEDLINE=93146981; PubMed=7844559;						RX MEDLINE=93146981; PubMed=7844559;						
Searched:	RA Ni H., Barrett A.D.;						RA Ni H., Barrett A.D.;						
Total number of hits satisfying chosen parameters:	RT "Nucleotide and deduced amino acid sequence of the structural protein genes of Japanese encephalitis viruses from different geographical locations";						RT "Nucleotide and deduced amino acid sequence of the structural protein genes of Japanese encephalitis viruses from different geographical locations";						
Minimum DB seq length: 0	RT LOC						RT LOC						
Maximum DB seq length: 2000000000	RJ Gen. Virol. 76:401-407 (1995).						RJ Gen. Virol. 76:401-407 (1995).						
Post-processing: Minimum Match 0%	EMBL; U03691; AAA67160; L-						EMBL; U03691; AAA67160; L-						
Maximum Match 100%	HSSP; Q88653; I0KE.						HSSP; Q88653; I0KE.						
Listing First 45 summaries	GO: GO:0019028; C:viral capsid; IEA.						GO: GO:0019028; C:viral capsid; IEA.						
Database :	GO: GO:0005198; F:viral envelope; IEA.						GO: GO:0005198; F:viral envelope; IEA.						
1: uniprot_sprot;*	GO: GO:0019058; P:viral infection cycle; IEA.						GO: GO:0019058; P:viral infection cycle; IEA.						
2: uniprot_trembl;*	InterPro; IPR01122; Flavi_capsid.						InterPro; IPR01122; Flavi_capsid.						
Scoring table: BL05UM62	InterPro; IPR000336; Flavi_glycoprote.						InterPro; IPR000336; Flavi_glycoprote.						
Gapop 10.0 , Gapext 0.5	InterPro; IPR00069; Flavi_M.						InterPro; IPR00069; Flavi_M.						
Searched:	InterPro; IPR01535; Flavi_propep.						InterPro; IPR01535; Flavi_propep.						
Total number of hits satisfying chosen parameters:	Pfam; PF01003; Flavi_capsid; 1.						Pfam; PF01003; Flavi_capsid; 1.						
Minimum DB seq length: 0	PF00869; Flavi_glycoprot; 1.						PF00869; Flavi_glycoprot; 1.						
Maximum DB seq length: 2000000000	PF02832; Flavi_glycop_C; 1.						PF02832; Flavi_glycop_C; 1.						
Post-processing: Minimum Match 0%	Pfam; PF01004; Flavi_M; 1.						Pfam; PF01004; Flavi_M; 1.						
Maximum Match 100%	Pfam; PF01570; Flavi_propep; 1.						Pfam; PF01570; Flavi_propep; 1.						
Listing First 45 summaries	PolyProtein; PB001556; Flavi_glycoprotE; 1.						PolyProtein; PB001556; Flavi_glycoprotE; 1.						
Database :	KW PolyProtein.						KW PolyProtein.						
1: uniprot_sprot;*	FT NON_TER						FT NON_TER						
2: uniprot_trembl;*	789 AA; 85517 MW; E0DC176FDA561636 CRC64;						789 AA; 85517 MW; E0DC176FDA561636 CRC64;						
Scoring table: BL05UM62	SEQNCE						SEQNCE						
Gapop 10.0 , Gapext 0.5	Query Match Best Local Similarity 76.3%; Score 90; DB 2; Length 789;						Query Match Best Local Similarity 76.3%; Score 90; DB 2; Length 789;						
Searched:	Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;						Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;						
Total number of hits satisfying chosen parameters:	QY 5 SAGSIMMWLASLAVVACAGA 24						QY 5 SAGSIMMWLASLAVVACAGA 24						
Minimum DB seq length: 0	DB 108 NGGSIMMWLASLAVVACAGA 127						DB 108 NGGSIMMWLASLAVVACAGA 127						
Maximum DB seq length: 2000000000	RESULT 2						RESULT 2						
Post-processing: Minimum Match 0%	Q82860						Q82860						
Maximum Match 100%	ID Q82860						ID Q82860						
Listing First 45 summaries	AC Q82860;						AC Q82860;						

DT	01-NOV-1996 (TREMBLrel. 01, Created)	DR	GO; GO:0005198; F:structural molecule activity; IBA.
DT	01-NOV-2004 (TREMBLrel. 26, Last annotation update)	DR	GO; GO:0019058; P:viral infectious cycle; IBA.
DT	Polyprotein (Fragment).	DR	InterPro; IPR001122; Flavi_capsidC.
DE	Japanese encephalitis virus.	DR	InterPro; IPR000336; Flavi_glycoprote.
OS	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;	DR	InterPro; IPR00069; Flavi_M.
OC	Flavivirus.	DR	InterPro; IPR002535; Flavi_propep.
OC	Flavivirus.	DR	Pfam; PF01003; Flavi_capsid; 1.
OX	NCBI_TaxID=11072;	DR	Pfam; PF00869; Flavi_glycoprot; 1.
RN	[1]	DR	Pfam; PF02832; Flavi_glycop_C; 1.
RP	SEQUENCE FROM N.A.	DR	Pfam; PF01004; Flavi_M; 1.
RC	STRAIN=SA14-2-8;	DR	Pfam; PF01570; Flavi_propep; 1.
RX	Medline=9267439; PubMed=8207417;	DR	ProDom; PD001556; Flavi_glycoprote;
RA	Ni H., Burns N.J., Chang G.J., Zhang M.J., Wills M.R., Trent D.W.,	FT	NON TER
RA	Sanders P.G., Barrett A.D.	FT	789
RA	"Comparison of nucleotide and deduced amino acid sequence of the 5' non-coding region and structural protein genes of the wild-type Japanese encephalitis virus strain SA14 and its attenuated vaccine derivatives."	FT	SEQUENCE 789 AA; 85842 MW; C055C3905F12C051 CRC64;
RT	Japanese encephalitis virus strain SA14 and its attenuated vaccine	Query Match	75.4%; Score 89; DB 2; Length 789;
RT	RL J. Gen. Virol. 75:1505-1510(1994).	Best Local Similarity 100.0%; Pred. No. 0.0002;	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	EMBL; U02267; AAA52215.1; -.	Db	7 GSIMMILASLAVVIACAGA 24
DR	DR HSSP; Q8853; IOKE.	Db	110 GSIMMILASLAVVIACAGA 127
DR	GO; GO:0019028; C:viral capsid; IBA.		
DR	GO; GO:0019031; C:viral envelope; IBA.		
DR	GO; GO:0019058; P:viral infectious cycle; IBA.		
DR	InterPro; IPR001122; Flavi_capsidC.	RESULT 4	
DR	InterPro; IPR000336; Flavi_glycoprote.	Q82865	PRELIMINARY; PRT; 789 AA.
DR	InterPro; IPR00069; Flavi_M.	AC	Q82865; PRELIMINARY; PRT; 789 AA.
DR	InterPro; IPR002535; Flavi_propep.	DT	01-NOV-1996 (TREMBLrel. 01, Created)
DR	Pfam; PF01003; Flavi_capsid; 1.	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DR	Pfam; PF00869; Flavi_glycoprot; 1.	DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DR	Pfam; PF00832; Flavi_glycop_C; 1.	DB	Polyprotein (Fragment).
DR	Pfam; PF01004; Flavi_M; 1.	DB	DBP
DR	Pfam; PF0570; Flavi_propep; 1.	DB	Japanese encephalitis virus.
DR	ProDom; PD001556; Flavi_glycoprote; 1.	OS	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
KW	Polyprotein.	OC	Flavivirus.
FT	NON TER	OC	Flavivirus.
SQ	SEQUENCE 789 AA; 85592 MW; 1A61502D9B53068E CRC64;	NCBI_TaxID=11072;	OX
Qy	7 GSIMMILASLAVVIACAGA 24	RN [1]	RN
Db	110 GSIMMILASLAVVIACAGA 127	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
		RC STRAIN=KPO034-35CT;	RC STRAIN=KPO034-35CT;
		RX MEDLINE=95146381; PubMed=7844559;	RX MEDLINE=95146381; PubMed=7844559;
		RA Ni H., Barrett A.D.;	RA Ni H., Barrett A.D.;
		RT "Nucleotide and deduced amino acid sequence of the structural protein genes of Japanese encephalitis viruses from different geographical locations,"	RT "Nucleotide and deduced amino acid sequence of the structural protein genes of Japanese encephalitis viruses from different geographical locations,"
		RL J. Gen. Virol. 76:401-407(1995).	RL J. Gen. Virol. 76:401-407(1995).
		DR PIR; U03693; AAA67162.1; -.	DR PIR; U03693; AAA67162.1; -.
		DR HSSP; Q8853; IOKE.	DR HSSP; Q8853; IOKE.
		DR GO; GO:0019028; C:viral envelope; IBA.	DR GO; GO:0019028; C:viral envelope; IBA.
		DR GO; GO:0005198; F:structural molecule activity; IBA.	DR GO; GO:0005198; F:structural molecule activity; IBA.
		DR GO; GO:0019058; P:viral infectious cycle; IBA.	DR GO; GO:0019058; P:viral infectious cycle; IBA.
		DR InterPro; IPR001122; Flavi_capsidC.	DR InterPro; IPR001122; Flavi_capsidC.
		DR InterPro; IPR000336; Flavi_glycoprote.	DR InterPro; IPR000336; Flavi_glycoprote.
		DR InterPro; IPR00069; Flavi_M.	DR InterPro; IPR00069; Flavi_M.
		DR InterPro; IPR002535; Flavi_propep.	DR InterPro; IPR002535; Flavi_propep.
		DR ProDom; PD001556; Flavi_glycoprote; 1.	DR ProDom; PD001556; Flavi_glycoprote; 1.
		KW Polyprotein.	KW Polyprotein.
		FT NON TER	FT NON TER
		SQ 7 GSIMMILASLAVVIACAGA 24	SQ 7 GSIMMILASLAVVIACAGA 24
		Query Match 75.4%; Score 89; DB 2; Length 789;	Query Match 75.4%; Score 89; DB 2; Length 789;
		Best Local Similarity 100.0%; Pred. No. 0.0002;	Best Local Similarity 100.0%; Pred. No. 0.0002;
		Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches	18;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Db	110	GSIMWLASLAVVIACAGA 127							
RESULT 8									
ID	Q86862	PRELIMINARY;	PRT;	793 AA.					
AC	Q86862;								
DR	01-NOV-1996 (TRIMBLrel. 01, Created) 01-MAR-2004 (TRIMBLrel. 26, Last annotation update)								
RA	"Comparison of nucleotide and deduced amino acid sequence of the 5'-non-coding region and structural protein genes of the wild-type Japanese encephalitis virus strain SA14 and its attenuated vaccine derivatives.";								
RA	RL J. Gen. Virol. 75:1505-1510(1994).								
RA	DR EMBL; U04521; AAA67173.1; -.								
RA	DR HSSP; Q88653; 10KB.								
RA	DR PIR; B44055; B44055.								
RA	DR GO; GO:0019038; C:viral capsid; IEA.								
RT	DR GO; GO:0019031; C:viral envelope; IEA.								
RT	DR GO; GO:0005198; F:structural molecule activity; IEA.								
RT	DR GO; GO:0019058; P:virial infectious cycle; IEA.								
RT	DR InterPro; IPR001122; Flavi_glycoprotE.								
RT	DR InterPro; IPR000336; Flavi_glycoprotE.								
RT	DR InterPro; IPR000659; Flavi_glycoprotE.								
RT	DR InterPro; IPR002535; Flavi_propep.								
RT	DR PF01003; Flavi_capsid; 1.								
RT	DR Pfam; PF00869; Flavi_glycoprot; 1.								
RT	DR PF02832; Flavi_glycop_C; 1.								
RT	DR PF01004; Flavi_M; 1.								
RT	DR PF01570; Flavi_propep; 1.								
RT	DR ProDom; PD001556; Flavi_glycoprote; 1.								
RT	DR KW Polypeptide.								
FT	FT CHAIN 1 127 C.								
FT	FT CHAIN 128 294 C.								
FT	FT CHAIN 295 >794 prM/M.								
FT	FT NON-TER 794 794 E.								
SQ	SQ SEQUENCE 794 AA; 86318 MW; 5E4400B2011c3581 CRC64;								
Qy	Query Match 75.4%; Score 89; DB 2; Length 794; Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSIMWLASLAVVIACAGA 127								
RESULT 10									
Qy	Query Match 75.4%; Score 89; DB 2; Length 793; Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSIMWLASLAVVIACAGA 24								
Db	109 GSIMWLASLAVVIACAGA 126								
RESULT 9									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSIMWLASLAVVIACAGA 24								
Db	109 GSIMWLASLAVVIACAGA 126								
RESULT 10									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSIMWLASLAVVIACAGA 127								
RESULT 11									
Qy	Query Match 75.4%; Score 89; DB 2; Length 793; Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSIMWLASLAVVIACAGA 24								
Db	110 GSIMWLASLAVVIACAGA 127								
RESULT 12									
Qy	Query Match 75.4%; Score 89; DB 2; Length 793; Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSIMWLASLAVVIACAGA 24								
Db	109 GSIMWLASLAVVIACAGA 126								
RESULT 13									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 14									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 15									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 16									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 17									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 18									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 19									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 20									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 21									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 22									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 23									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 24									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 25									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 26									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 27									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 28									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 29									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 30									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 31									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 32									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 33									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 34									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 35									
Qy	Query Match 75.4%; Score 89; DB 2; Length 794 AA. Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Db	7 GSTIMWLASLAVVIACAGA 24								
Db	110 GSTIMWLASLAVVIACAGA 127								
RESULT 36									

FT	PROPEP	54	146	Envelope glycoprotein M.	FT	CHAIN	795	1146	nonstructural protein 2.
FT	CHAIN	147	222	Major envelope protein E.	FT	CHAIN	1147	1373	nonstructural protein 2A.
FT	CHAIN	223	794	Nonstructural protein NS1.	FT	CHAIN	1374	1504	nonstructural protein 2B.
FT	CHAIN	795	1136	Nonstructural protein NS1.	FT	CHAIN	128	294	membrane protein precursor.
FT	CHAIN	1137	1301	Nonstructural protein NS2A.	FT	CHAIN	220	294	membrane protein.
FT	CHAIN	1302	1432	Flavivirin protease subunit NS2B.	FT	CHAIN	295	794	membrane protein.
FT	CHAIN	1433	>1440	Flavivirin protease subunit NS3.	FT	SEQUENCE	1504	AA;	envelope protein.
FT	DISULFID	225	252	By similarity.	FT	SEQUENCE	1504	AA;	101EB22FCDA1601 CRC64;
FT	DISULFID	282	338	By similarity.	Query Match				Score 89; DB 2; Length 1504;
FT	DISULFID	296	327	By similarity.	Best Local Similarity	100.0%	Pred. No.	0.00033	;
FT	DISULFID	314	343	By similarity.	Matches	18;	Conservative	0;	Mismatches 0;
FT	DISULFID	412	509	By similarity.	Indels	0;	Gaps	0;	
FT	DISULFID	526	557	By similarity.	Qy	7	GSIMMWLASLAVIACAGA 24		
FT	CARBOHYD	68	68	N-linked (GICNAC. . .) (Potential).	Db	110	GSIMMWLASLAVIACAGA 127		
FT	CARBOHYD	376	376	N-linked (GICNAC. . .) (Potential).					
FT	CARBOHYD	852	852	N-linked (GICNAC. . .) (Potential).					
FT	CARBOHYD	929	929	N-linked (GICNAC. . .) (Potential).					
FT	NON TER	1440	1440	158184 MN;	RESULT 14				
SQ	SEQUENCE	1440	AA;	4D489A36A3C2E6E CRC64;	POLG_JAEVI				
Query Match					POLG_JAEVI	STANDARD;			
Best Local Similarity	100.0%				POLG_JAEVI	PRT;	3432	AA.	
Matches	18;				POLG_JAEVI	PRT;	3432	AA.	
Qy	7	GSIMMWLASLAVIACAGA 24			POLG_JAEVI	PRT;	3432	AA.	
Db	36	GSIMMWLASLAVIACAGA 53			POLG_JAEVI	PRT;	3432	AA.	
RESULT 13					POLG_JAEVI	PRT;	3432	AA.	
Q04092					POLG_JAEVI	PRT;	3432	AA.	
AC	Q04092,				POLG_JAEVI	PRT;	3432	AA.	
DT	01-NOV-1996	(TREMBLrel.	01,	Created)	POLG_JAEVI	PRT;	3432	AA.	
DT	01-MAR-2003	(TREMBLrel.	23,	Last sequence update)	POLG_JAEVI	PRT;	3432	AA.	
DT	01-MAR-2004	(TREMBLrel.	26,	Last annotation update)	POLG_JAEVI	PRT;	3432	AA.	
DB	Polypeptide (Fragment).				POLG_JAEVI	PRT;	3432	AA.	
OS	Japanese encephalitis virus.				POLG_JAEVI	PRT;	3432	AA.	
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;				POLG_JAEVI	PRT;	3432	AA.	
OC	Flavivirus.				POLG_JAEVI	PRT;	3432	AA.	
DR	HSSP; Q88633; I0KE.				POLG_JAEVI	PRT;	3432	AA.	
DR	GO; GO:0019028; C: viral capsid; IEA.				POLG_JAEVI	PRT;	3432	AA.	
DR	GO; GO:0019031; C: viral envelope; IEA.				POLG_JAEVI	PRT;	3432	AA.	
DR	GO; GO:0019198; : structural molecule activity; IEA.				POLG_JAEVI	PRT;	3432	AA.	
DR	PFam; PF00058; P: viral infectious cycle; IEA.				POLG_JAEVI	PRT;	3432	AA.	
DR	InterPro; IPR001122; Flavi_glycoprotC.				POLG_JAEVI	PRT;	3432	AA.	
DR	InterPro; IPR000356; Flavi_glycoprotE.				POLG_JAEVI	PRT;	3432	AA.	
DR	InterPro; IPR000669; Flavi_M.				POLG_JAEVI	PRT;	3432	AA.	
DR	InterPro; IPR000157; Flavi_NS1.				POLG_JAEVI	PRT;	3432	AA.	
DR	InterPro; IPR000752; Flavi_NS2A.				POLG_JAEVI	PRT;	3432	AA.	
DR	InterPro; IPR000487; Flavi_NS2B.				POLG_JAEVI	PRT;	3432	AA.	
DR	InterPro; IPR002535; Flavi_propep.				POLG_JAEVI	PRT;	3432	AA.	
DR	DR InterPro; IPR00103; Flavi_capsid; 1.				POLG_JAEVI	PRT;	3432	AA.	
DR	PFam; PF00469; Flavi_glycoprot; 1.				POLG_JAEVI	PRT;	3432	AA.	
DR	PFam; PF02332; Flavi_glycop_1; 1.				POLG_JAEVI	PRT;	3432	AA.	
DR	PFam; PF01004; Flavi_M; 1.				POLG_JAEVI	PRT;	3432	AA.	
DR	PFam; PF00948; Flavi_NS1; 1.				POLG_JAEVI	PRT;	3432	AA.	
DR	PFam; PF00002; Flavi_NS2B; 1.				POLG_JAEVI	PRT;	3432	AA.	
DR	PFam; PF01570; Flavi_propep; 1.				POLG_JAEVI	PRT;	3432	AA.	
DR	Prod0n; P0001556; Flavi_glycoprotE; 1.				POLG_JAEVI	PRT;	3432	AA.	
DR	Prod0n; P001436; Flavi_NS1; 1.				POLG_JAEVI	PRT;	3432	AA.	
KW	Polymerase.				POLG_JAEVI	PRT;	3432	AA.	
FT	NON TER	1	1	capsid protein.	POLG_JAEVI	PRT;	3432	AA.	
FT	CHAIN	2	105		POLG_JAEVI	PRT;	3432	AA.	

Query Match Score 89; DB 2; Length 1504; Best Local Similarity 100.0%; Pred. No. 0.00033; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GSIMMWLASLAVIACAGA 24

Db 110 GSIMMWLASLAVIACAGA 127

RESULT 14

POLG_JAEVI STANDARD; PRT; 3432 AA.

POLG_JAEVI PRT; 3432 AA.

Query Match Score 89; DB 1; Length 3432;
Best Local Similarity 100.0%; Pred. No. 0.00065;

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7 GSIMWLASLAWVIACAGA 24
11.8 GSIMWLASLAWVIACAGA 127

Search completed: October 26, 2005, 01:34:30
Job time: 171 secs

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	28	43.5	36.9	245	4	US-09-963-137-190
OM protein - protein search, using sw model		29	43.5	36.9	253	4	US-09-468-554A-2
Run on:	October 26, 2005, 01:25:30 (without alignments)	30	43.5	36.9	256	4	US-09-468-554A-2
Title:	US-09-826-115A-14	31	43	36.4	106	4	US-09-621-916-4047
Perfect score:	118	32	43	36.4	246	1	US-09-902-540-14183
Sequence:	1 MGKRSAGSIMMILASLAVVIACAGA 24	33	43	36.4	333	1	US-08-440-556A-4
Scoring table:	BLOSUM62	34	43	36.4	562	4	US-09-902-540-10175
Searched:	513545 seqs, 74649064 residues	35	43	36.4	739	4	US-09-328-352-6048
Total number of hits satisfying chosen parameters:	513545	36	43	36.4	770	4	US-09-252-991A-24516
Minimum DB seq length: 0		37	42.5	36.0	257	4	US-09-1988-A
Maximum DB seq length: 200000000		38	42	35.6	118	4	US-09-039A-3080
Post-processing: Minimum Match 0%		39	42	35.6	143	4	US-09-270-567-60062
		40	42	35.6	156	4	US-09-270-767-44615
		41	42	35.6	161	2	US-08-368-552-2
		42	42	35.6	161	2	US-08-525-940-2
		43	42	35.6	161	2	US-08-976-838-2
		44	42	35.6	225	4	US-09-270-767-60537
		45	42	35.6	227	4	US-09-585-174-5
ALIGNMENTS							
Database :	Issued Patents AA:*						
	1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep:*						
	2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep:*						
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	6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*						
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES							
Result No.	Score	Query Match	Length	DB ID	Description		
1	78	66.1	32	4	US-09-452-638-56	Sequence 56, App1	
2	78	66.1	970	6	5229293-2	Patent No. 5229293	
3	78	66.1	970	6	5229293-2	Patent No. 5229293	
4	50	42.4	385	4	US-09-711-164-393	Sequence 393, App	
5	50	42.4	443	4	US-09-328-552-7059	Sequence 7059, App	
6	48	40.7	493	4	US-09-489-339A-13709	Sequence 13709, A	
7	48	40.7	510	4	US-09-543-681A-6077	Sequence 6077, App	
8	48	40.7	587	4	US-09-115-933-4	Sequence 4, App1	
9	46	39.0	27	3	US-08-905-723-344	Sequence 344, App	
10	46	39.0	129	4	US-08-602-787A-420	Sequence 420, App	
11	46	39.0	337	1	US-08-440-556A-3	Sequence 3, App1	
12	46	39.0	396	4	US-09-602-787A-118	Sequence 418, App	
13	45	39.0	414	4	US-09-489-039A-10428	Sequence 10428, A	
14	45	38.1	526	3	US-08-817-441-46	Sequence 46, App1	
15	44.5	38.1	877	3	US-08-817-441-102	Sequence 102, App	
16	44.5	37.7	253	4	US-09-963-137-198	Sequence 198, App	
17	44	37.3	76	3	US-09-227-357-255	Sequence 255, App	
18	44	37.3	267	4	US-09-252-991A-19626	Sequence 19626, A	
19	44	37.3	268	4	US-09-489-039A-11078	Sequence 11078, A	
20	44	37.3	289	4	US-09-252-991A-27680	Sequence 27680, A	
21	44	37.3	425	4	US-09-543-881A-6042	Sequence 6042, App	
22	44	37.3	486	4	US-09-543-681A-6238	Sequence 6238, App	
23	44	37.3	727	1	US-08-424-24B-2	Sequence 2, App1	
24	44	37.3	727	5	PCT-US94-05363A-2	Sequence 2, App1	
25	44	37.3	984	4	US-10-101-464A-919	Sequence 919, App	
26	44	37.3	1293	4	US-09-252-991A-11576	Sequence 17576, A	
27	43.5	241	4	US-09-468-554A-15	Sequence 15, App1		

Query Match 66.1%; Score 78; DB 6; Length 970;
 Best Local Similarity 94.4%; Pred. No. 0.0016;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SEQ ID NOS: 8252

Query Match 7 GSIMWLASLAVVIACAGA 24
 Best Local Similarity 94.4%; Pred. No. 0.0016;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 SEQ ID NOS: 52293-2

Query Match 5 SAGSIMWLASLAVVIACAG 23
 Best Local Similarity 42.1%; Pred. No. 1.3;
 Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

RESULT 6
 US-09-489-039A-13709
 Sequence 13709, Application US/09489039A

GENERAL INFORMATION:
 APPLICANT: Gary Breton et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709-2004-001
 CURRENT APPLICATION NUMBER: US/09/489, 039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO: 13709
 LENGTH: 493
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae

Query Match 60.7%; Score 48; DB 4; Length 493;
 Best Local Similarity 50.0%; Pred. No. 30;
 Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Query Match 9 IMWLASLAVVIACAGA 24
 Best Local Similarity 50.0%; Pred. No. 30;
 Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

RESULT 7
 US-09-489-039A-13709
 Sequence 6077, Application US/09543681A

GENERAL INFORMATION:
 APPLICANT: GARY BRETON
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709-1002-001
 CURRENT APPLICATION NUMBER: US/09/543, 681A
 CURRENT FILING DATE: 2000-04-05
 PRIOR APPLICATION NUMBER: US 60/128, 706
 PRIOR FILING DATE: 1999-04-09
 SEQ ID NO: 6077
 LENGTH: 510
 TYPE: PRT
 ORGANISM: Proteus mirabilis

Query Match 40.7%; Score 48; DB 4; Length 510;
 Best Local Similarity 56.2%; Pred. No. 31;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Query Match 9 IMWLASLAVVIACAGA 24
 Best Local Similarity 50.0%; Pred. No. 30;
 Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

RESULT 8
 US-09-328-352-7069
 Sequence 7069, Application US/09128352
 Patent No. 6662958
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC99-03PA
 CURRENT APPLICATION NUMBER: US/09/328, 352
 CURRENT FILING DATE: 1999-06-04

Query Match 42.4%; Score 50; DB 4; Length 385;
 Best Local Similarity 37.5%; Pred. No. 11;
 Matches 9; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Query Match 1 NGKRSAGSIMWLASLAVVIACAGA 24
 Best Local Similarity 37.5%; Pred. No. 11;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Query Match 103 LARTSLGSGFWAAALLALLACSDA 126
 Best Local Similarity 37.5%; Pred. No. 11;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

RESULT 9
 US-09-328-352-7069
 Sequence 7069, Application US/09128352
 Patent No. 6662958
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC99-03PA
 CURRENT APPLICATION NUMBER: US/09/328, 352
 CURRENT FILING DATE: 1999-06-04

Query Match 40.7%; Score 48; DB 4; Length 510;
 Best Local Similarity 56.2%; Pred. No. 31;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Query Match 9 IMWLASLAVVIACAGA 24
 Best Local Similarity 50.0%; Pred. No. 30;
 Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Query Match 111 LWWLASLAVVIACFCSA 126
 Best Local Similarity 50.0%; Pred. No. 30;
 Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

RESULT 8
US-09-815-923-4
Sequence 4, Application US/09815523
; Patent No. 6787642
; GENERAL INFORMATION:
; APPLICANT: Gill, Sarjeet S.
; APPLICANT: Ross, Linda S.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. 6787642e1
; TITLE OF INVENTION: Target Sites for Insecticides
; FILE REFERENCE: 023070-093000US
; CURRENT APPLICATION NUMBER: US/09/815,923
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 587
; TYPE: PRT
; ORGANISM: Manduca sexta
; FEATURE:
; OTHER INFORMATION: serotonin transporter
US-09-815-923-4
Query Match 40.7%; Score 48; DB 4; Length 587;
Best Local Similarity 53.3%; Pred. No. 36;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 2 GGRSAGSIMWASLA 16
Db 232 GVRSAKGKVWVTLA 246

RESULT 9
US-09-905-223-344
Sequence 344, Application US/08905223
; Patent No. 6722029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duepert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 344:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:

RESULT 10
US-09-602-787A-420
; Sequence 420, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Krug, Burkhard
; APPLICANT: Schider, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US/09/60141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932160.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932237.3
; PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19933005.0
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: DE 19933006.9
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: DE 19940764.9
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: DE 19940765.7
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: DE 19940766.5
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: DE 19940830.0
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: DE 19940831.9
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: DE 19940832.7
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: DE 19940833.5
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: DE 19941378.9
 PRIOR FILING DATE: 1999-08-31
 PRIOR APPLICATION NUMBER: DE 19941379.7
 PRIOR FILING DATE: 1999-08-31
 PRIOR APPLICATION NUMBER: DE 19941395.9
 PRIOR FILING DATE: 1999-08-31
 PRIOR APPLICATION NUMBER: DE 19942077.7
 PRIOR FILING DATE: 1999-09-03
 PRIOR APPLICATION NUMBER: DE 19942078.5
 PRIOR FILING DATE: 1999-09-03
 PRIOR APPLICATION NUMBER: DE 19942079.3
 PRIOR FILING DATE: 1999-09-03
 PRIOR APPLICATION NUMBER: DE 19942088.2
 PRIOR FILING DATE: 1999-09-03
 NUMBER OF SEQ ID NOS: 678
 SEQ ID NO 420
 LENGTH: 129
 TYPE: PRT
 ORGANISM: *Corynebacterium glutamicum*
 US-09-602-787A-420

Query Match 39.0%; Score 46; DB 4; Length 129;
 Best Local Similarity 36.4%; Pred. No. 13;
 Matches 8; Conservative 7; Mismatches 7; Indels 0;
 Gaps 0;

RESULT 11
 US-08-440-856A-3
 Sequence 3; Application US/08440856A
 Patent No. 5150873
 GENERAL INFORMATION:
 APPLICANT: DELLAPORTA, STEPHEN L.
 TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESS: MORRISON & FOERSTER
 STREET: 2000 PENNSYLVANIA AVE. N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/440,856A
 FILING DATE: 15-MAY-1995
 CLASSIFICATION: 800
 PRIOR FILING DATE: 1999-07-09

ATTORNEY/AGENT INFORMATION:
 NAME: MILLMAN, ROBERT A.
 REGISTRATION NUMBER: 36,217
 REFERENCE/DOCKET NUMBER: 05463-20001.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1517
 TELEX: (202) 887-0763
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 337 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-440-856A-3

Query Match 39.0%; Score 46; DB 1; Length 337;
 Best Local Similarity 47.8%; Pred. No. 39;
 Matches 11; Conservative 4; Mismatches 8; Indels 0;
 Gaps 0;

Qy 1 MGKRSAGSIMMLASLAVVIAGAG 23
 Db 181 MAPRPRGGIVSVASVAAVLGGLG 203

RESULT 12
 US-09-602-787A-418
 Sequence 418; Application US/09602787A
 Patent No. 6696561
 GENERAL INFORMATION:
 APPLICANT: Pompejus, Mark
 APPLICANT: Kr"ger, Burkhard
 APPLICANT: Sch"fer, Hartwig
 APPLICANT: Zelder, Oskar
 APPLICANT: Haberhauer, Gregor
 TITLE OF INVENTION: *CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE TRANSPORT*
 TITLE OF INVENTION:
 TITLE OF INVENTION:
 FILE REFERENCE: EGG-125CP
 CURRENT APPLICATION NUMBER: US/09/602,787A
 CURRENT FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US/99/60/141031
 PRIOR FILING DATE: 1999-06-25
 PRIOR APPLICATION NUMBER: DE 19931454.3
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931478.0
 PRIOR FILING DATE: 1999-07-08
 PRIOR APPLICATION NUMBER: DE 19931563.9
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932122.1
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932124.8
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932125.6
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932128.0
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932180.9
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932209.0
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932212.0
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932227.9
 PRIOR FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: DE 19932228.7
 PRIOR FILING DATE: 1999-07-09

Prior Application Number: DE 19932229.5
 Prior Filing Date: 1993-07-09
 Prior Application Number: DE 19932230.9
 Prior Filing Date: 1993-07-09
 Prior Application Number: DE 19932927.3
 Prior Filing Date: 1993-07-14
 Prior Application Number: DE 19933005.0
 Prior Filing Date: 1993-07-14
 Prior Application Number: DE 19933006.9
 Prior Filing Date: 1993-07-14
 Prior Application Number: DE 19940764.9
 Prior Filing Date: 1993-08-27
 Prior Application Number: DE 19940765.7
 Prior Filing Date: 1993-08-27
 Prior Application Number: DE 19940766.5
 Prior Filing Date: 1993-08-27
 Prior Application Number: DE 19940830.0
 Prior Filing Date: 1993-08-27
 Prior Application Number: DE 19940831.9
 Prior Filing Date: 1993-08-27
 Prior Application Number: DE 19940832.7
 Prior Filing Date: 1993-08-27
 Prior Application Number: DE 19940833.5
 Prior Filing Date: 1993-08-27
 Prior Application Number: DE 19941378.9
 Prior Filing Date: 1993-08-31
 Prior Application Number: DE 19941379.7
 Prior Filing Date: 1993-08-31
 Prior Application Number: DE 19941395.9
 Prior Filing Date: 1993-08-31
 Prior Application Number: DE 19942077.7
 Prior Filing Date: 1993-09-03
 Prior Application Number: DE 19942078.5
 Prior Filing Date: 1993-09-03
 Prior Application Number: DE 19942079.3
 Prior Filing Date: 1993-09-03
 Prior Application Number: DE 19942088.2
 Prior Filing Date: 1993-09-03
 Number of SEQ ID NOS: 678
 SEQ ID NO 418
 LENGTH: 396
 TYPE: PRT
 ORGANISM: Corynebacterium glutamicum
 US-09-602-78A-418

Query Match 39.0%; Score 46; DB 4; Length 396;
 Best Local Similarity 36.4%; Fred. No. 47;
 Matches 8; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MGKRSAGGSIMPLASLAVIACCA 22
 Db 304 IGLRIFGAVLWASISVIGGS 325

RESULT 13
 US-09-489-039A-10428
 / Sequence 10428, Application US/09489039A
 / Patent No. 6610836
 / GENERAL INFORMATION:
 / APPLICANT: Gary Bretton et. al
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 / TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 / FILE REFERENCE: 2709.2004001
 / CURRENT APPLICATION NUMBER: US/09/489,039A
 / CURRENT FILING DATE: 2000-01-27
 / PRIOR APPLICATION NUMBER: US 60/117,747
 / PRIOR FILING DATE: 1999-01-29
 / NUMBER OF SEQ ID NOS: 14342
 / LENGTH: 414
 / TYPE: PRT
 / ORGANISM: Klebsiella pneumoniae

Query Match 38.1%; Score 45; DB 3; Length 526;
 Best Local Similarity 42.9%; Fred. No. 92;
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MGKRSAGGSIMPLASLAVIAC 21
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Db 8 MGKRNRKLGIVCLLALIIPC 28

RESULT 15
 US-08-817-441-102
 / Sequence 102; Application US/08817441
 / Patent No. 6,99294
 GENERAL INFORMATION:
 / / APPLICANT: CHARNEAU, PIERRE
 / / CLAVEL, FRANCOISE
 / / BORMAN, ANDREW
 / / APPLICANT: QUILLET, CAROLINE
 / / GUSTARD, DENISE
 / / MONTAGNER, LUC
 / / APPLICANT: DONJON DE SAINT-MARTIN, JACQUELINE
 / / APPLICANT: COHEN, JAQUES
 / / TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
 / / TITLE OF INVENTION: SUBTYPE) ANTIGENS
 / / NUMBER OF SEQUENCES: 103
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ADDRESSEE: Dunner, L.L.P.
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/817,441
 FILING DATE: 11-JUL-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR 95/01391
 FILING DATE: 20-OCT-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 9412554
 FILING DATE: 20-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 9502526
 FILING DATE: 03-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Meyers, Kenneth J.
 REGISTRATION NUMBER: 25,146
 REFERENCE DOCKET NUMBER: 03260.6005-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 102:
 / / SEQUENCE CHARACTERISTICS:
 / / LENGTH: 877 amino acids
 / / TYPE: amino acid
 / / STRANGENESS: single
 / / TOPOLOGY: linear
 / / MOLECULE TYPE: protein
 / / US-08-817-441-102

Query Match 38.1%; Score 45; DB 3; Length 877;
 Best Local Similarity 42.9%; Pred. No. 1.6e+02;
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 Qy 1 MGKRNRKLGIVCLLALIIPC 21
 Db 8 MGKRNRKLGIVCLLALIIPC 28

Search completed: October 26, 2005, 01:36:01
 Job time: 43 secs

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OM protein - protein search, using sw model

Run on: October 26, 2005, 01:34:40 ; Search time 163 Seconds (without alignments)

61,474 Million cell updates/sec

Title: US-09-826-115A-14

Perfect score: 118

Sequence: 1 MGKRSAGSIMWLASLAVVIACAGA 24

Scoring table: BLOSUM62

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Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

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RESULT 1

US-09-826-115-14

Sequence 14, Application US/09826115

Publication No. US20030022849A1

GENERAL INFORMATION:

APPLICANT: Chang, Gwong-Jen J

TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of Flavivirus Infection

FILE REFERENCE: 141114-03203

CURRENT APPLICATION NUMBER: US/09-826,115

CURRENT FILING DATE: 2001-04-04

PRIOR APPLICATION NUMBER: pct/us99/12298

PRIOR FILING DATE: 1999-06-03

PRIOR APPLICATION NUMBER: 09/701,536

PRIOR FILING DATE: 2000-11-29

PRIOR APPLICATION NUMBER: 60/087,908

PRIOR FILING DATE: 1998-06-04

NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 14

LENGTH: 24

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of artificial sequence; note =

OTHER INFORMATION: Synthetic construct

OTHER INFORMATION: JE Signal

US-09-826-115-14

Query Match 100.0% ; Score 118; DB 10; Length 24;

Best Local Similarity 100.0% ; Pred. No. 2.5e-10;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGKRSAGSIMWLASLAVVIACAGA 24

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	118	100.0	24	18	US-10-500-796A-14
3	118	100.0	33	18	US-10-500-796A-37
4	118	100.0	685	18	US-10-500-796A-43
5	118	100.0	685	18	US-10-500-796A-45
6	118	100.0	695	18	US-10-500-796A-47
7	118	100.0	692	10	US-09-826-115-16
8	96	81.0	692	18	US-10-500-796A-16
9	96	81.0	24	10	US-09-826-115-27
10	96	81.4	24	18	US-10-500-796A-27
11	96	81.4	681	10	US-09-826-115-20

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence; note = synthetic construct
US-10-500-796A-37

RESULT 2
; Sequence 14, Application US/10500796A
; Publication No. US2005163804A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; represented by the Secretary of the Department of Health and
; Human Services, Centers for Disease Control and Prevention
; APPLICANT: Chang, Gwong-Jen J.
; APPLICANT: Human Services, Centers for Disease Control and Prevention
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
; FILE REFERENCE: 6395-64909-02
; CURRENT APPLICATION NUMBER: US/10/500/796A
; PRIOR APPLICATION NUMBER: PCT/US02/10764
; CURRENT FILING DATE: 2004-07-06
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/826,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO: 14
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence; note = synthetic construct
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: JF Signal
US-10-500-796A-14

Query 1 MGKRSAGSIMMLASLAVIACAGA 24
Db 1 MGKRSAGSIMMLASLAVIACAGA 24

RESULT 3
; Sequence 37, Application US/10500796A
; Publication No. US2005163804A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; represented by the Secretary of the Department of Health and
; Human Services, Centers for Disease Control and Prevention
; APPLICANT: Chang, Gwong-Jen J.
; APPLICANT: Human Services, Centers for Disease Control and Prevention
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
; FILE REFERENCE: 6395-64909-02
; CURRENT APPLICATION NUMBER: US/10/500/796A
; PRIOR APPLICATION NUMBER: PCT/US02/10764
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/825,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/12298
; PRIOR FILING DATE: 1998-06-03
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO: 33
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence; note = synthetic construct
US-10-500-796A-37

Query 1 MGKRSAGSIMMLASLAVIACAGA 24
Db 1 MGKRSAGSIMMLASLAVIACAGA 24

RESULT 4
; Sequence 43, Application US/10500796A
; Publication No. US20050163804A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; represented by the Secretary of the Department of Health and
; Human Services, Centers for Disease Control and Prevention
; APPLICANT: Chang, Gwong-Jen J.
; APPLICANT: Human Services, Centers for Disease Control and Prevention
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
; FILE REFERENCE: 6395-64909-02
; CURRENT APPLICATION NUMBER: US/10/500/796A
; PRIOR APPLICATION NUMBER: PCT/US02/10764
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/826,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO: 43
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-500-796A-43

Query 1 MGKRSAGSIMMLASLAVIACAGA 24
Db 1 MGKRSAGSIMMLASLAVIACAGA 24

RESULT 5
; Sequence 45, Application US/10500796A
; Publication No. US20050163804A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; represented by the Secretary of the Department of Health and
; Human Services, Centers for Disease Control and Prevention
; APPLICANT: Chang, Gwong-Jen J.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
; FILE REFERENCE: 6395-64909-02
; CURRENT APPLICATION NUMBER: US/10/500/796A
; PRIOR APPLICATION NUMBER: PCT/US02/10764
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/825,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/12298
; PRIOR FILING DATE: 1998-06-03
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO: 45
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-500-796A-45

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; PRIOR APPLICATION NUMBER: PCT/US02/10764
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/826,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-500-796A-45

Query Match
Best Local Similarity 100.0%; Pred. No. 7e-09; Length 685;
Matches 24; Conservative 0; Mismatches 0; Gaps 0;
Db 1 MGKRSAGSIMMLASLAVIACAGA 24
1 MGKRSAGSIMMLASLAVIACAGA 24

RESULT 6
US-10-500-796A-47
; Sequence 47, Application US/10500796A
; Publication No. US2005163804A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
;           represented by the Secretary of the Department of Health and
;           Human Services, Centers for Disease Control and Prevention
;           Chang, Gwong-Jen J.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
FILE REFERENCE: 6395-64909-02
CURRENT FILING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: PCT/US02/10764
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 09/826,115
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: PCT/US99/12298
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.3
SEQ ID NO 47
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-500-796A-47

Query Match
Best Local Similarity 100.0%; Pred. No. 7e-09; Length 685;
Matches 24; Conservative 0; Mismatches 0; Gaps 0;
Db 1 MGKRSAGSIMMLASLAVIACAGA 24
1 MGKRSAGSIMMLASLAVIACAGA 24

RESULT 7
US-09-826-115-16

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Qy 1 MGKRSAGSIMMLASLAVVIACAGA 24
 Db 1 MGKRSAGSIMMLASLAVVIACAGA 24

RESULT 9
 US-09-826-115-27
 ; Sequence 27, Application US/09826115
 ; Publication No. US2003022849A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chang, Gwong-Jen J
 ; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of
 ; Flavivirus Infection
 ; FILE REFERENCE: 14114 0332U3
 ; CURRENT APPLICATION NUMBER: US/09/826,115
 ; CURRENT FILING DATE: 2001-04-04
 ; PRIOR APPLICATION NUMBER: pct/us99/12298
 ; PRIOR FILING DATE: 1999-06-13
 ; PRIOR APPLICATION NUMBER: 09/701,536
 ; PRIOR FILING DATE: 2000-11-29
 ; PRIOR APPLICATION NUMBER: 60/087,908
 ; PRIOR FILING DATE: 1998-06-04
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 24
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of artificial sequence; note =
 ; OTHER INFORMATION: synthetic construct
 ; OTHER INFORMATION: Modified JE Signal
 ; OTHER INFORMATION: US-09-826-115-27

Query Match 81.4%; Score 96; DB 10; Length 24;
 Best Local Similarity 87.5%; Pred. No. 4.7e-07;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGKRSAGSIMMLASLAVVIACAGA 24
 Db 1 MGKRSAGSIMMLASLAVVIAGTSA 24

RESULT 10
 US-10-500-796A-27
 ; Sequence 27, Application US/10500796A
 ; Publication No. US2005016380A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Government of the United States of America, as
 ; represented by the Secretary of the Department of Health and
 ; Human Services, Centers for Disease Control and Prevention
 ; APPLICANT: Chang, Gwong-Jen J.
 ; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
 ; FILE REFERENCE: 6395-64909-02
 ; CURRENT APPLICATION NUMBER: US/10/500,796A
 ; CURRENT FILING DATE: 2004-07-06
 ; PRIOR APPLICATION NUMBER: pct/us02/10764
 ; PRIOR FILING DATE: 2002-04-04
 ; PRIOR APPLICATION NUMBER: 09/826,115
 ; PRIOR FILING DATE: 2001-04-04
 ; PRIOR APPLICATION NUMBER: 09/701,536
 ; PRIOR FILING DATE: 2000-11-29
 ; PRIOR APPLICATION NUMBER: pct/us99/12298
 ; PRIOR FILING DATE: 1999-06-03
 ; PRIOR APPLICATION NUMBER: 60/087,908
 ; PRIOR FILING DATE: 1998-06-04
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 27
 ; LENGTH: 24
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

OTHER INFORMATION: Description of artificial sequence; note =
 OTHER INFORMATION: synthetic construct
 ; OTHER INFORMATION: US-09-826-115-27

Query Match 81.4%; Score 96; DB 10; Length 681;
 Best Local Similarity 87.5%; Pred. No. 1.3e-05;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGKRSAGSIMMLASLAVVIACAGA 24
 Db 1 MGKRSAGSIMMLASLAVVIAGTSA 24

RESULT 12
 US-09-826-115-24
 ; Sequence 24, Application US/09826115
 ; Publication No. US20030022849A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chang, Gwong-Jen J
 ; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of
 ; Flavivirus Infection
 ; FILE REFERENCE: 14114 0332U3
 ; CURRENT APPLICATION NUMBER: US/09/826,115
 ; CURRENT FILING DATE: 2001-04-04
 ; PRIOR APPLICATION NUMBER: pct/us99/12298
 ; PRIOR FILING DATE: 1999-06-03
 ; PRIOR APPLICATION NUMBER: 09/701,536
 ; PRIOR FILING DATE: 2000-11-29
 ; PRIOR APPLICATION NUMBER: 60/087,908
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 24
 ; LENGTH: 681

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of artificial sequence; note =
; OTHER INFORMATION: Synthetic construct
US-09-826-115-24

Query Match 81.4%; Score 96; DB 10; Length 681;
Best Local Similarity 87.5%; Pred. No. 1.3e-05;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Software: PatentIn version 3.3
SEQ ID NO 20
Db 1 MGKRSAGSIMMLASLAVIACAGA 24
        1 MGKRSAGSIMMLASLAVIAGTSA 24
        ; TYPE: PRT
        ; ORGANISM: Artificial Sequence
        ; FEATURE:
        ; OTHER INFORMATION: Synthetic Construct
US-10-500-796A-20

RESULT 13
US-10-500-796A-24
; Sequence 24, Application US/10500796A
; Publication No. US20050163804A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
;             represented by the Secretary of the Department of Health and
;             Human Services, Centers for Disease Control and Prevention
;             Chang, Gwong-Jen J.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
; FILE REFERENCE: 6395-64909-02
; CURRENT APPLICATION NUMBER: US/10/500,796A
; CURRENT FILING DATE: 2004-07-06
; PRIOR APPLICATION NUMBER: PCT/US02/10764
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/826,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 61
; Software: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-500-796A-24

Query Match 81.4%; Score 96; DB 18; Length 681;
Best Local Similarity 87.5%; Pred. No. 1.3e-05;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Software: PatentIn version 3.3
SEQ ID NO 20
Db 1 MGKRSAGSIMMLASLAVIACAGA 24
        1 MGKRSAGSIMMLASLAVIAGTSA 24
        ; TYPE: PRT
        ; ORGANISM: Artificial Sequence
        ; FEATURE:
        ; OTHER INFORMATION: Synthetic Construct
US-09-826-115-22

RESULT 15
US-09-826-115-22
; Sequence 22, Application US/09826115
; Publication No. US20030022849A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Gwong-Jen J.
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of
;             Flavivirus Infection
; FILE REFERENCE: 14114.033203
; CURRENT APPLICATION NUMBER: US/09/826,115
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 31
; Software: FastSEQ for Windows Version 4.0
SEQ ID NO 22
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence; note =
; OTHER INFORMATION: synthetic construct
US-09-826-115-22

Query Match 81.4%; Score 96; DB 10; Length 692;
Best Local Similarity 87.5%; Pred. No. 1.3e-05;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Software: FastSEQ for Windows Version 4.0
SEQ ID NO 22
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence; note =
; OTHER INFORMATION: synthetic construct
US-09-826-115-22

RESULT 14
US-10-500-796A-20
; Sequence 20, Application US/10500796A
; Publication No. US20050163804A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
;             represented by the Secretary of the Department of Health and
;             Human Services, Centers for Disease Control and Prevention
;             Chang, Gwong-Jen J.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
; FILE REFERENCE: 6395-64909-02
; CURRENT APPLICATION NUMBER: US/10/500,796A
; CURRENT FILING DATE: 2004-07-06
; PRIOR APPLICATION NUMBER: PCT/US02/10764
; PRIOR FILING DATE: 2002-04-04

Search completed: October 26, 2005, 01:48:45
Job time : 164 secs

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